

# Cloning immunoglobulin variable domains for expression by the polymerase chain reaction

(chimeric antibodies/MBr1)

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**cDNA Synthesis and Amplification.** RNA was prepared from about  $5 \times 10^8$  hybridoma cells grown in roller bottles, and mRNA was selected on oligo(dT)-cellulose (25). First-strand cDNA synthesis was based on ref. 26. A 50- $\mu$ l reaction mixture containing 10  $\mu$ g of mRNA, 20 pmol of VH1FOR primer [5'-d(TGAGGAGACGGTGACCGTGGTCCCTTGGCCCCAG)] or VK1FOR primer [5'-d(GTTAGATCTCCAGCTTGGTCCC)], 250  $\mu$ M of each dNTP, 10 mM dithiothreitol, 100 mM Tris-HCl (pH 8.3), 10 mM MgCl<sub>2</sub>, and 140 mM KCl was heated at 70°C for 10 min and cooled. Reverse transcriptase (Anglian Biotech, Colchester, U.K.) was added (46 units) and incubated at 42°C for 1 hr. For amplification with a thermostable DNA polymerase (15), a 50- $\mu$ l reaction mixture containing 5  $\mu$ l of the cDNA-RNA hybrid, 25 pmol of primers VH1FOR or VK1FOR and VH1BACK [5'-d(AGGTSMARCTGCAGSAGTCWGG) in which S = C or G, M = A or C, R = A or G, and W = A or T] or VK1BACK [5'-d(GACATTCAGCTGACCCAGTCTCCA)] as appropriate, 250  $\mu$ M

of each dNTP, 67 mM Tris chloride (pH 8.8), 17 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 10 mM MgCl<sub>2</sub>, 200  $\mu$ g of gelatine per ml, and 2 units of thermus aquaticus (Taq) polymerase (Cetus) was overlaid with paraffin oil and subjected to 25 rounds of temperature cycling with a Techne PHC-1 programmable heating block. A typical cycle was 1 min at 95°C (denature), 1 min at 30°C (anneal), and 2 min at 72°C (elongate). The sample (and oil) was extracted twice with ether, once with phenol, and then with phenol/CHCl<sub>3</sub>, followed by ethanol precipitation. The sample was taken up in 50  $\mu$ l of water and frozen.

Table 1. Checking primers for mismatches with the data base entries

Primers	Entries with none, one, or two mismatches		
	0	1	2
VH1FOR	50/131	71/131	
VH1BACK	22/141	56/141	43/141
VK1FOR	38/61	20/61	
VK1BACK	19/115	54/115	26/115

For each primer, the number of entries with zero, one, or two mismatches with respect to the 14 nucleotides at the 3' end of each of the primers are given, as well as the total number of eligible entries. For the mixed VH1BACK primer, each of the possible variants was scored and the results summed.

*Handwritten note:* Here's more AA sequences at one end than at the other

*Handwritten note:* 110 AA  $\Rightarrow$  330 bases

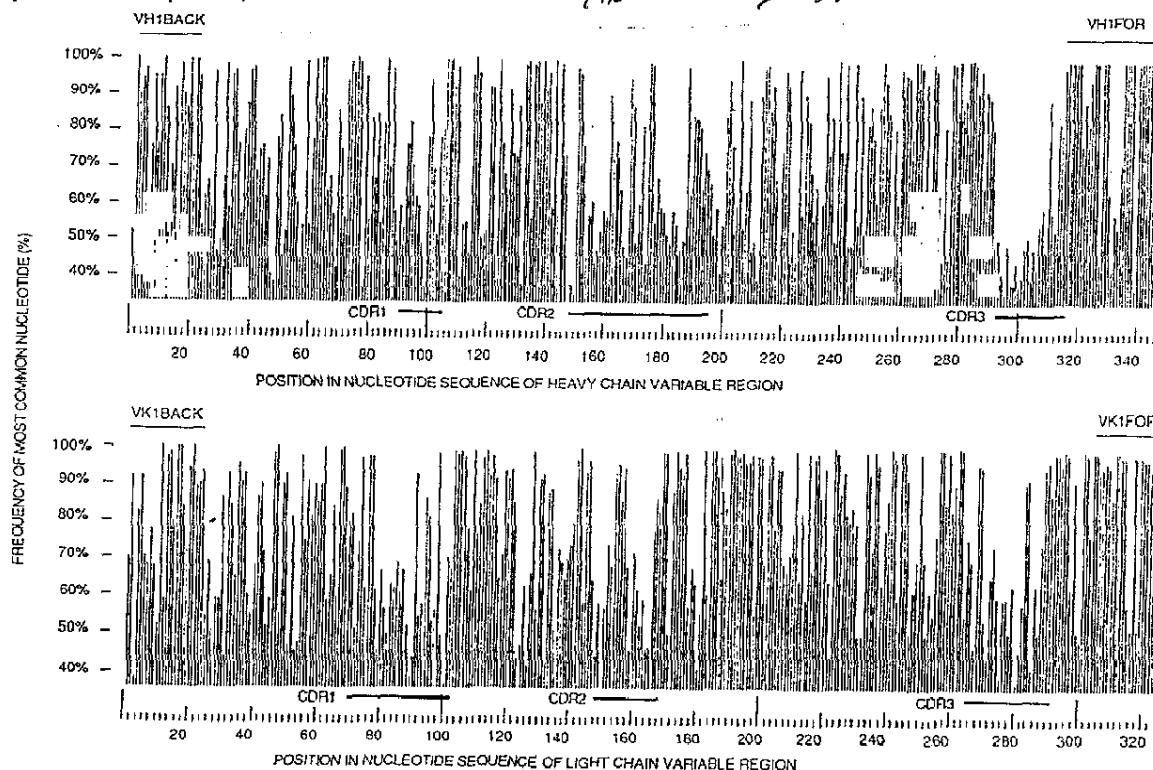


FIG. 1. Frequency of the most common nucleotides in V<sub>H</sub> and V<sub>L</sub> gene sequences in ref. 23. CDR1, CDR2, and CDR3 are located,

PM3001193190

Given primer sequence would probably be able to  
prime seq of many more V region  
sig of this link

GB 15

left join

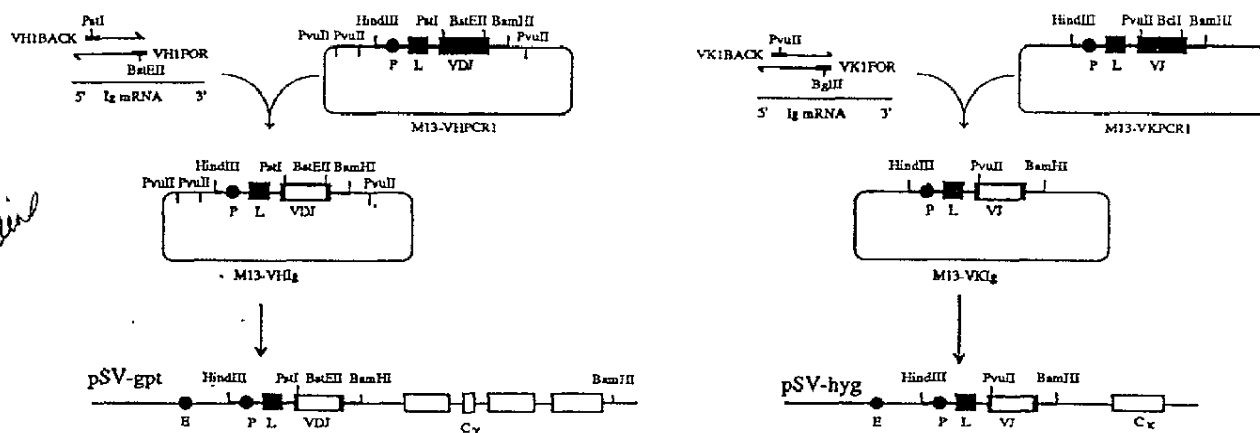


FIG. 2. Scheme for amplification of cDNA and cloning into phage M13 vectors to hook up V region genes for expression. The vectors M13-VHPCR1 and M13-VKPCR1, for cloning the amplified cDNA, contain introns; transcription is driven from the immunoglobulin heavy chain promoter (P), and the signal sequence (L) and leader intron are taken from the mouse V47 unrearranged  $V_H$  gene (12). The noncoding sequence to the 3' end of the  $V_H$  gene is described in ref. 12 and of the  $V_\kappa$  gene in ref. 9.

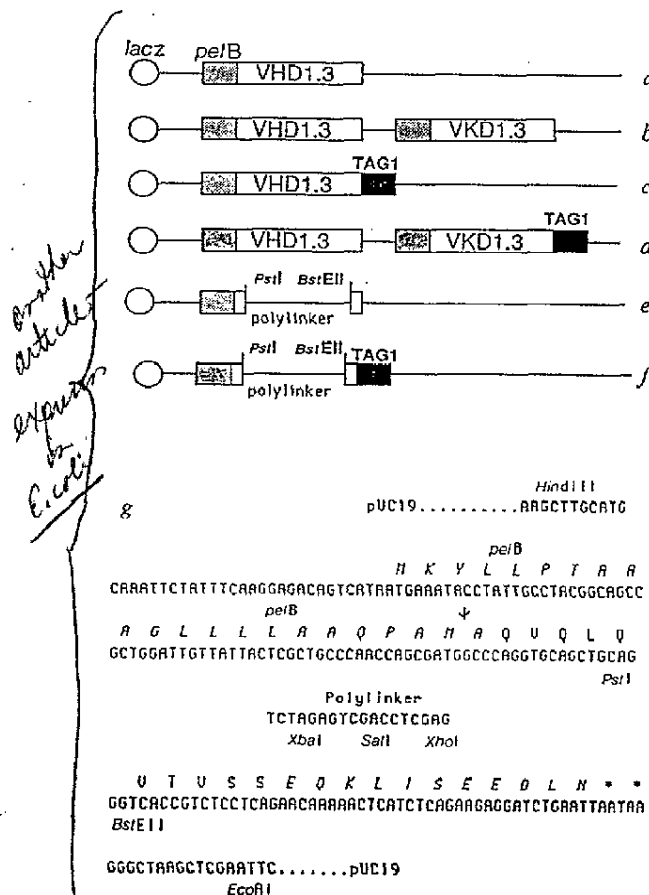
Bank made by PCR & directly into expression vector

1A .glu.val.gln.leu.gln.glu.ser.gly.pro.ser  
1B .gln.val.gln.leu.lys.glu.ser.gly.pro.gly  
IIA .glu.val.gln.leu.gln.gln.ser.gly.pro.glu  
IIB .gln.val.gln.leu.gln.gln.pro.gly.ala.glu  
IIC .glu.val.gln.leu.gln.gln.ser.gly.ala.glu  
IIIA .glu.val.lys.leu.val.glu.ser.gly.gly.gly  
IIIB .glu.val.lys.leu.leu.glu.ser.gly.gly.gly  
IIIC .glu.val.lys.leu.glu.glu.ser.gly.gly.gly  
IIID .glu.val.gln.leu.val.glu.ser.gly.gly.gly  
VA .glu.val.gln.leu.gln.gln.ser.gly.ala.glu  
VB .glu.val.gln.leu.gln.gln.ser.gly.ala.glu

AG.GTC.AAG.CTG.CAG.CAG.TCA.GG  
glu.val.gln.leu.gln.glu.ser.glu  
gln lys gln

Pst

Buell tried to repeat this & had some  
trouble. "Hibrid going round"  
is that some AB are easier  
than other



PM3001193191